

Table 1:NimaGen ESI-PATH panel content (Predictive Analysis for Therapy in Cancer)

Gene	RefSeq	Region of interest	Amplification detection*
AKT1	NM_005163.2	codon 17	
AKT2	NM_001626.5	codon 17	
AKT3	NM_181690.2	codon 17	
ALK	NM_004304.4	codon 1059-1150, 1173-1278	yes
ARAF	NM_001654.4	codon 214	
BRAF	NM_004333.4	codon 455-488, 566-580, 594-605	yes
DDR2	NM_006182.2	codon 503-856	
EGFR	NM_005228.4	codon 434-499, 688-875	yes
ERBB2	NM_004448.3	codon 310 650-883,	yes
FGFR1**	n/a	n/a	yes
FGFR2**	n/a	n/a	yes
FGFR3**	n/a	n/a	yes
GNA11	NM_002067.4	codon 183 and 209	
GNAQ	NM_002072.4	codon 183 and 209	
GNAS	NM_000516.5	codon 201 and 227	
HRAS	NM_005343.3	codon 12 13 59 and 61	
IDH1	NM_005896.3	codon 132	
IDH2	NM_002168.3	codon 140 and 172	
JAK2	NM_004972.3	codon 617	
KIT	NM_000222.2	codon 412-513, 550-591, 640-787, 799-850	yes
KRAS	NM_004985.4	codon 12 13 59 61 117 and 146	yes
MAP2K1	NM_002755.3	codon 28-231	
MDM2**	n/a	n/a	yes
MET	NM_001127500.2	codon 168 375 982-1027, 1230-1284, 1304	yes
MTOR	NM_004958.3	codon 1458-1489, 1789-1820, 1971-1995, 2194-2220, 2404-2433, 2484-2509	
NRAS	NM_002524.4	codon 12 13 59 61 117 and 146	
PDGFRA	NM_006206.5	codon 552-595, 632-667, 824-848	yes
PIK3CA	NM_006218.3	codon 345 420 539-554, 1043-1050	yes
POLE	NM_006231.3	codon 268-491	
PTEN	NM_000314.6	codon 86-267, 276-342	
RAF1	NM_002880.3	codon 257-261	
ROS1	NM_002944.2	codon 1927-2189	
TP53	NM_000546.5	>95% of coding sequences and splice sites (-5/+5)	

* Besides mutations this panel can also be used for detection of amplifications.

The sensitivity of this analysis is subject/depends of the percentage tumourcells.

** For these genes only amplifications can be detected and no sequence analysis can be performed.